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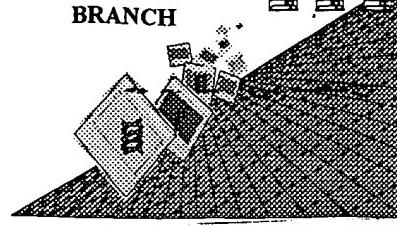
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RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/613,591

Source: BATCH

Date Processed by STIC: 11/30/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/613,591</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

BATCH

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/613,591

DATE: 11/30/2000
 TIME: 11:09:24

Input Set : A:\A-378CIP5 US.txt
 Output Set: N:\CRF3\11302000\I613591.raw

Does Not Comply
 Corrected Diskette Needed

```

3 <110> APPLICANT: BOYLE, WILLIAM
4   LACEY, DAVID
5   CALZONE, FRANK
6   CHANG, MING-SHI
7   SENALDI, GIORGIO
9 <120> TITLE OF INVENTION: COMBINATION THERAPY FOR CONDITIONS LEADING TO BONE LOSS
11 <130> FILE REFERENCE: A-378CIP5
13 <140> CURRENT APPLICATION NUMBER: US 09/613,591
14 <141> CURRENT FILING DATE: 2000-07-10
16 <150> PRTOR APPLICATION NUMBER: US 09/457,647
17 <151> PRIOR FILING DATE: 1999-12-09
19 <150> PRIOR APPLICATION NUMBER: US 09/350,670
20 <151> PRIOR FILING DATE: 1999-07-09
22 <150> PRIOR APPLICATION NUMBER: US 08/706,945
23 <151> PRTOR FILING DATE: 1996-09-03
25 <150> PRTOR APPLICATION NUMBER: US 08/577,788
26 <151> PRIOR FILING DATE: 1995-12-22
28 <160> NUMBER OF SEQ ID NOS: 168
30 <170> SOFTWARE: PatentIn version 3.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 36
34 <212> TYPE: DNA
35 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <221> NAME/KEY: misc_feature
39 <222> LOCATION: ()...()
40 <223> OTHER INFORMATION: Random cDNA primer with internal NotI restriction site.
43 <400> SEQUENCE: 1
W--> 44 aaaggaaagg aaaaagcggc cgctacannnn nnnnnn 36
47 <210> SEQ ID NO: 2
48 <211> LENGTH: 16
49 <212> TYPE: DNA
50 <213> ORGANISM: Artificial Sequence
52 <220> FEATURE:
53 <221> NAME/KEY: misc_feature
54 <222> LOCATION: ()...()
55 <223> OTHER INFORMATION: ds oligonucleotide adapter
58 <400> SEQUENCE: 2
59 tcgaccacacg cgtccg 16
62 <210> SEQ ID NO: 3
63 <211> LENGTH: 12
64 <212> TYPE: DNA
65 <213> ORGANISM: Artificial Sequence
67 <220> FEATURE:
68 <221> NAME/KEY: misc_feature
69 <222> LOCATION: ()...()
70 <223> OTHER INFORMATION: ds oligonucleotide adapter

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*see item 10
on Error summary
sheet*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/613,591

DATE: 11/30/2000
TIME: 11:09:24

Input Set : A:\A-378CIPS US.txt
Output Set: N:\CRF3\11302000\I613591.raw

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73 <400> SEQUENCE: 3
74 ggggtgcgcaag gc
77 <210> SEQ ID NO: 4
78 <211> LENGTH: 18
79 <212> TYPE: DNA
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <221> NAME/KEY: misc_feature
84 <222> LOCATION: ()..()
85 <223> OTHER INFORMATION: PCR primer
88 <400> SEQUENCE: 4
89 tqtaaaacga cggccaaqt
92 <210> SEQ ID NO: 5
93 <211> LENGTH: 18
94 <212> TYPE: DNA
95 <213> ORGANISM: Artificial Sequence
97 <220> FEATURE:
98 <221> NAME/KEY: misc_feature
99 <222> LOCATION: ()..()
100 <223> OTHER INFORMATION: PCR primer
103 <400> SEQUENCE: 5
104 caggaaacag ctatgacc
107 <210> SEQ ID NO: 6
108 <211> LENGTH: 20
109 <212> TYPE: DNA
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <221> NAME/KEY: misc_feature
114 <222> LOCATION: ()..()
115 <223> OTHER INFORMATION: T3 primer
118 <400> SEQUENCE: 6
119 caaittaaccc tcactaaagg
122 <210> SEQ ID NO: 7
123 <211> LENGTH: 23
124 <212> TYPE: DNA
125 <213> ORGANISM: Rattus rattus
127 <400> SEQUENCE: 7
128 gcatttatgac ccagaaaaccg gac
131 <210> SEQ ID NO: 8
132 <211> LENGTH: 23
133 <212> TYPE: DNA
134 <213> ORGANISM: Rattus rattus
136 <400> SEQUENCE: 8
137 aggttagcggcc cttccttcaca ttc
140 <210> SEQ ID NO: 9
141 <211> LENGTH: 30
142 <212> TYPE: DNA
143 <213> ORGANISM: Artificial Sequence
145 <220> FEATURE:

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/613,591

DATE: 11/30/2000
 TIME: 11:09:24

Input Set : A:\A-378CIPS US.txt
 Output Set: N:\CRF3\11302000\I613591.raw

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146 <221> NAME/KEY: misc_feature
147 <222> LOCATION: ()..()
148 <223> OTHER INFORMATION: PCR primer
151 <400> SEQUENCE: 9
152 gactagtccc acaaataaca agtggctgtg 30
155 <210> SEQ ID NO: 10
156 <211> LENGTH: 45
157 <212> TYPE: DNA
158 <213> ORGANISM: Artificial Sequence
160 <220> FEATURE:
161 <221> NAME/KEY: misc_feature
162 <222> LOCATION: ()..()
163 <223> OTHER INFORMATION: PCR primer
166 <400> SEQUENCE: 10
167 ataagaatgc ggccgtctaa ctagaaaca gcccagtgtac cattc 45
170 <210> SEQ ID NO: 11
171 <211> LENGTH: 21
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <221> NAME/KEY: misc_feature
177 <222> LOCATION: ()..()
178 <223> OTHER INFORMATION: PCR primer
181 <400> SEQUENCE: 11
182 qcctctagaa agagctggaa c 21
185 <210> SEQ ID NO: 12
186 <211> LENGTH: 21
187 <212> TYPE: DNA
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <221> NAME/KEY: misc_feature
192 <222> LOCATION: ()..()
193 <223> OTHER INFORMATION: PCR primer
196 <400> SEQUENCE: 12
197 cgccgtgttc catttatgag c 21
200 <210> SEQ ID NO: 13
201 <211> LENGTH: 24
202 <212> TYPE: DNA
203 <213> ORGANISM: Rattus rattus
205 <400> SEQUENCE: 13
206 atcaaaggca gggcatactt cctg 24
209 <210> SEQ ID NO: 14
210 <211> LENGTH: 24
211 <212> TYPE: DNA
212 <213> ORGANISM: Rattus rattus
214 <400> SEQUENCE: 14
215 gtgcactcc tggttcacgg tctg .24
218 <210> SEQ ID NO: 15
219 <211> LENGTH: 24

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/613,591

DATE: 11/30/2000
TIME: 11:09:24

Input Set : A:\A-378CIPS US.txt
Output Set: N:\CRF3\11302000\I613591.raw

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220 <212> TYPE: DNA
221 <213> ORGANISM: Rattus rattus
223 <400> SEQUENCE: 15
224 caagacacct tgaaggccct gatg 24
227 <210> SEQ ID NO: 16
228 <211> LENGTH: 24
229 <212> TYPE: DNA
230 <213> ORGANISM: Rattus rattus
232 <400> SEQUENCE: 16
233 taactttac agaagagcat cagc 24
236 <210> SEQ ID NO: 17
237 <211> LENGTH: 33
238 <212> TYPE: DNA
239 <213> ORGANISM: Rattus rattus
241 <400> SEQUENCE: 17
242 agcgcggccg catqaacaag tggctgtgct gcg 33
245 <210> SEQ ID NO: 18
246 <211> LENGTH: 31
247 <212> TYPE: DNA
248 <213> ORGANISM: Rattus rattus
250 <400> SEQUENCE: 18
251 agctcttagag aaacagccca gtgaccatcc c 31
254 <210> SEQ ID NO: 19
255 <211> LENGTH: 24
256 <212> TYPE: DNA
257 <213> ORGANISM: Rattus rattus
259 <400> SEQUENCE: 19
260 gtgaagctgt gcaagaacct gatg 24
263 <210> SEQ ID NO: 20
264 <211> LENGTH: 24
265 <212> TYPE: DNA
266 <213> ORGANISM: Rattus rattus
268 <400> SEQUENCE: 20
269 atcaaaggca gggcatactt cctg 24
272 <210> SEQ ID NO: 21
273 <211> LENGTH: 24
274 <212> TYPE: DNA
275 <213> ORGANISM: Homo sapiens
277 <400> SEQUENCE: 21
278 cagatccctga agctgctcag ttty 24
281 <210> SEQ ID NO: 22
282 <211> LENGTH: 33
283 <212> TYPE: DNA
284 <213> ORGANISM: Homo sapiens
286 <400> SEQUENCE: 22
287 agcgcggccg cggggaccac aatgaacaag ttg 33
290 <210> SEQ ID NO: 23
291 <211> LENGTH: 33
292 <212> TYPE: DNA

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/613,591

DATE: 11/30/2000
TIME: 11:09:24

Input Set : A:\A-378CIP5 US.txt
Output Set: N:\CRF3\11302000\1613591.raw

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293 <213> ORGANISM: Homo sapiens
295 <400> SEQUENCE: 23
296 aqctctagaat ttgtgaaac acagctcaat ggc          33
299 <210> SEQ ID NO: 24
300 <211> LENGTH: 39
301 <212> TYPE: DNA
302 <213> ORGANISM: Artificial Sequence
304 <220> FEATURE:
305 <221> NAME/KEY: misc_feature
306 <222> LOCATION: ()..()
307 <223> OTHER INFORMATION: PCR primer
310 <400> SEQUENCE: 24
311 atagcgcccg ctgagccaa atcttgtac aaaaactcac      39
314 <210> SEQ ID NO: 25
315 <211> LENGTH: 45
316 <212> TYPE: DNA
317 <213> ORGANISM: Artificial Sequence
319 <220> FEATURE:
320 <221> NAME/KEY: misc_feature
321 <222> LOCATION: ()..()
322 <223> OTHER INFORMATION: PCR primer
325 <400> SEQUENCE: 25
326 tcttagatcg acttattcatt tacccggaga cagggagagg ctatt      45
329 <210> SEQ ID NO: 26
330 <211> LENGTH: 38
331 <212> TYPE: DNA
332 <213> ORGANISM: Mus musculus
334 <400> SEQUENCE: 26
335 cctctqaqct caagcttccg aggaccacaa tgaacaag      38
338 <210> SEQ ID NO: 27
339 <211> LENGTH: 43
340 <212> TYPE: DNA
341 <213> ORGANISM: Mus musculus
343 <400> SEQUENCE: 27
344 cctctgcggc cgcttaagcag cttatccca cgatttgaac ctg      43
347 <210> SEQ ID NO: 28
348 <211> LENGTH: 38
349 <212> TYPE: DNA
350 <213> ORGANISM: Mus musculus
352 <400> SEQUENCE: 28
353 cctctqaqct caagcttccg aggaccacaa tgaacaag      38
356 <210> SEQ ID NO: 29
357 <211> LENGTH: 24
358 <212> TYPE: DNA
359 <213> ORGANISM: Homo sapiens
361 <400> SEQUENCE: 29
362 tccgttaagaa acagccccgt gacc      24
365 <210> SEQ ID NO: 30
366 <211> LENGTH: 31

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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/613,591

DATE: 11/30/2000
TIME: 11:09:25

Input Set : A:\A-378CIPS US.txt
Output Set: N:\CRF3\11302000\I613591.raw

L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1